RAW SEQUENCE LISTING

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Application Serial Number: _10/509,565A_

Source: _PU_

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RAW SEQUENCE LISTING   DATE: 07/19/2005
PATENT APPLICATION: **US/10/509,565A**   TIME: 08:52:52

Input Set : **A:\10-509,565 Sequence Listing.txt**
Output Set: **N:\CRF4\07192005\J509565A.raw**

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 3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
 4       TAKEDA, Masayoshi
 5       ABE, Kunitake
 6       YAMAJI, Noboru
 8 <120> TITLE OF INVENTION: NOVEL PROMOTER
10 <130> FILE REFERENCE: Q83865
12 <140> CURRENT APPLICATION NUMBER: 10/509,565A
13 <141> CURRENT FILING DATE: 2004-09-29
15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07807
16 <151> PRIOR FILING DATE: 2003-06-19
18 <150> PRIOR APPLICATION NUMBER: JP 2002-180543
19 <151> PRIOR FILING DATE: 2002-06-20
21 <160> NUMBER OF SEQ ID NOS: 33
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 3675
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(3675)
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38 1               5                   10                  15
40 ctg ttg gcg cag gtg gcc gag cag gca cct gcg tgc gcc atg gga ccc      96
41 Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
42               20                  25                  30
44 gca gcg gca gcg cct ggg agc ccg agc gtc ccg cgt cct cct cca ccc     144
45 Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro Pro
46               35                  40                  45
48 gcg gag cgg ccg ggc tgg atg gaa aag ggc gaa tat gac ctg gtc tct     192
49 Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
50     50                  55                  60
52 gcc tac gag gtt gac cac agg ggc gat tac gtg tcc cat gaa atc atg     240
53 Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
54 65                  70                  75                  80
56 cac cat cag cgg cgg aga aga gca gtg gcc gtg tcc gag gtt gag tct     288
57 His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser Glu Val Glu Ser
58               85                  90                  95
60 ctt cac ctt cgg ctg aaa ggc tcc agg cac gac ttc cac gtg gat ctg     336
61 Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Val Asp Leu
62               100                 105                 110
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 64 agg act tcc agc agc cta gtg gct cct ggc ttt att gtg cag acg ttg    384
 65 Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
 66         115                 120                 125
 68 gga aag aca ggc act aag tct gtg cag act tta ccg cca gag gac ttc    432
 69 Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
 70         130                 135                 140
 72 tgt ttc tat caa ggc tct ttg cga tca cac aga aac tcc tca gtg gcc    480
 73 Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
 74 145                 150                 155                 160
 76 ctt tca acc tgc caa ggc ttg tca ggc atg ata cga aca gaa gag gca    528
 77 Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
 78                 165                 170                 175
 80 gat tac ttc cta agg cca ctt cct tca cac ctc tca tgg aaa ctc ggc    576
 81 Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
 82             180                 185                 190
 84 aga gct gcc caa ggc agc tcg cca tcc cac gta ctg tac aag aga tcc    624
 85 Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
 86         195                 200                 205
 88 aca gag ccc cat gct cct ggg gcc agt gag gtc ctg gtg acc tca agg    672
 89 Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
 90         210                 215                 220
 92 aca tgg gag ctg gca cat caa ccc ctg cac agc agc gac ctt cgc ctg    720
 93 Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
 94 225                 230                 235                 240
 96 gga ctg cca caa aag cag cat ttc tgt gga aga cgc aag aaa tac atg    768
 97 Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
 98                 245                 250                 255
100 ccc cag cct ccc aag gaa gac ctc ttc atc ttg cca gat gag tat aag    816
101 Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
102             260                 265                 270
104 tct tgc tta cgg cat aag cgc tct ctt ctg agg tcc cat aga aat gaa    864
105 Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
106         275                 280                 285
108 gaa ctg aac gtg gag acc ttg gtg gtg gtc gac aaa aag atg atg caa    912
109 Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
110         290                 295                 300
112 aac cat ggc cat gaa aat atc acc acc tac gtg ctc acg ata ctc aac    960
113 Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
114 305                 310                 315                 320
116 atg gta tct gct tta ttc aaa gat gga aca ata gga gga aac atc aac   1008
117 Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
118                 325                 330                 335
120 att gca att gta ggt ctg att ctt cta gaa gat gaa cag cca gga ctg   1056
121 Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
122             340                 345                 350
124 gtg ata agt cac cac gca gac cac acc tta agt agc ttc tgc cag tgg   1104
125 Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
126         355                 360                 365
128 cag tct gga ttg atg ggg aaa gat ggg act cgt cat gac cac gcc atc   1152
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129 Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
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132 tta ctg act ggt ctg gat ata tgt tcc tgg aag aat gag ccc tgt gac    1200
133 Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
134 385             390             395             400
136 act ttg gga ttt gca ccc ata agt gga atg tgt agt aaa tat cgc agc    1248
137 Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
138             405             410             415
140 tgc acg att aat gaa gat aca ggt ctt gga ctg gcc ttc acc att gcc    1296
141 Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
142             420             425             430
144 cat gag tct gga cac aac ttt ggc atg att cat gat gga gaa ggg aac    1344
145 His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn
146     435             440             445
148 atg tgt aaa aag tcc gag ggc aac atc atg tcc cct aca ttg gca gga    1392
149 Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly
150     450             455             460
152 cgc aat gga gtc ttc tcc tgg tca ccc tgc agc cgc cag tat cta cac    1440
153 Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His
154 465             470             475             480
156 aaa ttt cta agc acc gct caa gct atc tgc ctt gct gat cag cca aag    1488
157 Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys
158             485             490             495
160 cct gtg aag gaa tac aag tat cct gag aaa ttg cca gga gaa tta tat    1536
161 Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr
162     500             505             510
164 gat gca aac aca cag tgc aag tgg cag ttc gga gag aaa gcc aag ctc    1584
165 Asp Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu
166     515             520             525
168 tgc atg ctg gac ttt aaa aag gac atc tgt aaa gcc ctg tgg tgc cat    1632
169 Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His
170     530             535             540
172 cgt att gga agg aaa tgt gag act aaa ttt atg cca gca gca gaa ggc    1680
173 Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly
174 545             550             555             560
176 aca att tgt ggg cat gac atg tgg tgc cgg gga gga cag tgt gtg aaa    1728
177 Thr Ile Cys Gly His Asp Met Trp Cys Arg Gly Gly Gln Cys Val Lys
178             565             570             575
180 tat ggt gat gaa ggc ccc aag ccc acc cat ggc cac tgg tcg gac tgg    1776
181 Tyr Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp
182             580             585             590
184 tct tct tgg tcc cca tgc tcc agg acc tgc gga ggg gga gta tct cat    1824
185 Ser Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His
186             595             600             605
188 agg agt cgc ctc tgc acc aac ccc aag cca tcg cat gga ggg aag ttc    1872
189 Arg Ser Arg Leu Cys Thr Asn Pro Lys Pro Ser His Gly Gly Lys Phe
190     610             615             620
192 tgt gag ggc tcc act cgc act ctg aag ctc tgc aac agt cag aaa tgt    1920
193 Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys
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194 625                    630                    635                    640
196 ccc cgg gac agt gtt gac ttc cgt gct gct cag tgt gcc gag cac aac       1968
197 Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn
198                    645                    650                    655
200 agc aga cga ttc aga ggg cgg cac tac aag tgg aag cct tac act caa       2016
201 Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Tyr Thr Gln
202                    660                    665                    670
204 gta gaa gat cag gac tta tgc aaa ctc tac tgt atc gca gaa gga ttt       2064
205 Val Glu Asp Gln Asp Leu Cys Lys Leu Tyr Cys Ile Ala Glu Gly Phe
206             675                    680                    685
208 gat ttc ttc ttt tct ttg tca aat aaa gtc aaa gat ggg act cca tgc       2112
209 Asp Phe Phe Phe Ser Leu Ser Asn Lys Val Lys Asp Gly Thr Pro Cys
210         690                    695                    700
212 tcg gag gat agc cgt aat gtt tgt ata gat ggg ata tgt gag aga gtt       2160
213 Ser Glu Asp Ser Arg Asn Val Cys Ile Asp Gly Ile Cys Glu Arg Val
214 705                    710                    715                    720
216 gga tgt gac aat gtc ctt gga tct gat gct gtt gaa gac gtc tgt ggg       2208
217 Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val Glu Asp Val Cys Gly
218                    725                    730                    735
220 gtg tgt aac ggg aat aac tca gcc tgc acg att cac agg ggt ctc tac       2256
221 Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile His Arg Gly Leu Tyr
222             740                    745                    750
224 acc aag cac cac cac acc aac cag tat tat cac atg gtc acc att cct       2304
225 Thr Lys His His His Thr Asn Gln Tyr Tyr His Met Val Thr Ile Pro
226         755                    760                    765
228 tct gga gcc cgg agt atc cgc atc tat gaa atg aac gtc tct acc tcc       2352
229 Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn Val Ser Thr Ser
230 770                    775                    780
232 tac att tct gtg cgc aat gcc ctc aga agg tac tac ctg aat ggg cac       2400
233 Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr Leu Asn Gly His
234 785                    790                    795                    800
236 tgg acc gtg gac tgg ccc ggc cgg tac aaa ttt tcg ggc act act ttc       2448
237 Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser Gly Thr Thr Phe
238                    805                    810                    815
240 gac tac aga cgg tcc tat aat gag ccc gag aac tta atc gct act gga       2496
241 Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu Ile Ala Thr Gly
242             820                    825                    830
244 cca acc aac gag aca ctg att gtg gag ctg ctg ttt cag gga agg aac       2544
245 Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe Gln Gly Arg Asn
246         835                    840                    845
248 ccg ggt gtt gcc tgg gaa tac tcc atg cct cgc ttg ggg acc gag aag       2592
249 Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu Gly Thr Glu Lys
250 850                    855                    860
252 cag ccc cct gcc cag ccc agc tac act tgg gcc atc gtg cgc tct gag       2640
253 Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile Val Arg Ser Glu
254 865                    870                    875                    880
256 tgc tcc gtg tcc tgc gga ggg gga cag atg acc gtg aga gag ggc tgc       2688
257 Cys Ser Val Ser Cys Gly Gly Gly Gln Met Thr Val Arg Glu Gly Cys
258                    885                    890                    895
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260 tac aga gac ctg aag ttt caa gta aat atg tcc ttc tgc aat ccc aag   2736
261 Tyr Arg Asp Leu Lys Phe Gln Val Asn Met Ser Phe Cys Asn Pro Lys
262         900                 905                 910
264 aca cga cct gtc acg ggg ctg gtg cct tgc aaa gta tct gcc tgt cct   2784
265 Thr Arg Pro Val Thr Gly Leu Val Pro Cys Lys Val Ser Ala Cys Pro
266         915                 920                 925
268 ccc agc tgg tcc gtg ggg aac tgg agt gcc tgc agt cgg acg tgt ggc   2832
269 Pro Ser Trp Ser Val Gly Asn Trp Ser Ala Cys Ser Arg Thr Cys Gly
270         930                 935                 940
272 ggg ggt gcc cag agc cgc ccc gtg cag tgc aca cgg cgg gtg cac tat   2880
273 Gly Gly Ala Gln Ser Arg Pro Val Gln Cys Thr Arg Arg Val His Tyr
274 945                 950                 955                 960
276 gac tcg gag cca gtc ccg gcc agc ctg tgc cct cag cct gct ccc tcc   2928
277 Asp Ser Glu Pro Val Pro Ala Ser Leu Cys Pro Gln Pro Ala Pro Ser
278                 965                 970                 975
280 agc agg cag gcc tgc aac tct cag agc tgc cca cct gca tgg agc gcc   2976
281 Ser Arg Gln Ala Cys Asn Ser Gln Ser Cys Pro Pro Ala Trp Ser Ala
282         980                 985                 990
284 ggg ccc tgg gca gag tgc tca cac  acc tgt ggg aag ggg  tgg agg aag   3024
285 Gly Pro Trp Ala Glu Cys Ser His  Thr Cys Gly Lys Gly  Trp Arg Lys
286         995                 1000                 1005
288 cgg gca  gtg gcc tgt aag agc  acc aac ccc tcg gcc  aga gcg cag   3069
289 Arg Ala  Val Ala Cys Lys Ser  Thr Asn Pro Ser Ala  Arg Ala Gln
290     1010                 1015                 1020
292 ctg ctg  ccc gac gct gtc tgc  acc tcc gag ccc aag  ccc agg atg   3114
293 Leu Leu  Pro Asp Ala Val Cys  Thr Ser Glu Pro Lys  Pro Arg Met
294     1025                 1030                 1035
296 cat gaa  gcc tgt ctg ctt cag  cgc tgc cac aag ccc  aag aag ctg   3159
297 His Glu  Ala Cys Leu Leu Gln  Arg Cys His Lys Pro  Lys Lys Leu
298     1040                 1045                 1050
300 cag tgg  ctg gtg tcc gcc tgg  tcc cag tgc tct gtg  aca tgt gaa   3204
301 Gln Trp  Leu Val Ser Ala Trp  Ser Gln Cys Ser Val  Thr Cys Glu
302     1055                 1060                 1065
304 aga gga  aca cag aaa aga ttc  tta aaa tgt gct gaa  aag tat gtt   3249
305 Arg Gly  Thr Gln Lys Arg Phe  Leu Lys Cys Ala Glu  Lys Tyr Val
306     1070                 1075                 1080
308 tct gga  aag tat cga gag ctg  gcc tca aag aag tgc  tca cat ttg   3294
309 Ser Gly  Lys Tyr Arg Glu Leu  Ala Ser Lys Lys Cys  Ser His Leu
310     1085                 1090                 1095
312 ccg aag  ccc agc ctg gag ctg  gaa cgt gcc tgc gcc  ccg ctt cca   3339
313 Pro Lys  Pro Ser Leu Glu Leu  Glu Arg Ala Cys Ala  Pro Leu Pro
314     1100                 1105                 1110
316 tgc ccc  agg cac ccc cca ttt  gct gct gcg gga ccc  tcg agg ggc   3384
317 Cys Pro  Arg His Pro Pro Phe  Ala Ala Ala Gly Pro  Ser Arg Gly
318     1115                 1120                 1125
320 agc tgg  ttt gcc tca ccc tgg  tct cag tgc acg gcc  agc tgt ggg   3429
321 Ser Trp  Phe Ala Ser Pro Trp  Ser Gln Cys Thr Ala  Ser Cys Gly
322     1130                 1135                 1140
324 gga ggc  gtt cag acg agg tcc  gtg cag tgc ctg gct  ggg ggc cgg   3474
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/509,565A**

DATE: 07/19/2005
TIME: 08:52:53

Input Set : **A:\10-509,565 Sequence Listing.txt**
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